REMARKS

The specification has been amended to correct typographical and grammatical errors, and the claims have been amended to clarify the invention. Specifically, the specification has been amended in the Table at the bottom of page 8 to correct misalignments in the columns of the Table. Claim 1 has been amended to recite a specific antigenic fragment of SEQ ID NO:1 and a naturally occurring variant of SEQ ID NO:1 having at least 95% identity to SEQ ID NO:1. Support for the amendments to claim 1 is found in the specification, for example, at p. 3, lines 24-25, at p. 8, lines 13-19, and at p. 9, lines 29-31. No new matter is added by these amendments, and entry of the amendments is therefore requested.

Restriction Requirement

In the Restriction Requirement, the Examiner requested Applicants to elect one of the following inventions:

Group I (claims 1-7) drawn to polynucleotides, vectors, host cells and a recombinant method of producing a protein.

Group II (claims 8-11) drawn to a method for detecting expression or differential expression of nucleic acids in a sample.

Group III (claims 12 and 13) drawn to a method of using cDNA to screen a plurality of molecules or compounds.

Group IV (claims 14, 15 and 22) drawn to polypeptides.

Group V (claims 16 and 17) drawn to a method of using a protein to screen compounds to identify a ligand.

Group VI (claims 18 and 19) drawn to antibodies and methods of making antibodies.

Group VII (claims 20 and 21) drawn to a method of using an antibody to diagnose disease conditions.

Group VIII (claim 22) drawn to a method of treating rheumatoid arthritis comprising administering a polypeptide of Group IV.

Applicants hereby elect, with traverse, to prosecute Group I, which includes and is drawn to Claims 1-7. Applicants submit that claims 8-11 of Group II and claims 12 and 13 of Group III are methods of use of the polynucleotides of Group I that are limited in scope to the composition of matter of these claims and could therefore be examined together with the claims of Group I without undue burden. It is noted that Group I already contains a method of use of the polynucleotide in making a protein (claim 7), and that the Examiner has also included a method of use of the polypeptides of the invention in Group IV (claim 22) together with the compositions of matter of the polypeptides and therefore does not consider the examination of method claims and composition of matter claims together in those instances to be an undue burden.

Accordingly, applicants ask reconsideration of the Restriction Requirement and examination of claims1-13 in Groups I-III. In the event the Examiner maintains the Restriction Requirement, Applicants reserve the right to prosecute the subject matter of non-elected claims in subsequent divisional applications.

Applicants believe that no fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Deposit Account No. 09-0108.

Respectfully submitted,

INCYTE GENOMICS, INC.

Date: February 21, 2003

David G. Streeter, Ph.D.
Reg. No. 43,168
Direct Dial Telephone: (650) 845-5741

3160 Porter Drive
Palo Alto, California 94304
Phone: (650) 855-0555
Fax: (650) 849-8886

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Paragraph(s) beginning at line 29 of page 8 has been amended as follows:

SEQ ID	cDNA	Length	Nt_H Alignment	Library
3	8113313H1	392	1-392	OSTEUNC01
4	8235763H1	526	33-558	OSTEUNC01
5	4048821H1	301	494-794	SINTNOT18
6	2105134H1	135	538-672	BRAITUT03
7	7716364H1	651	629-1277	SINTFEE02[SINTFEE02]
8	8234468H1	574	804-1378	OSTEUNC01
[OSTEUNC01]				
9	7716340H1	425	853-1277	SINTFEE02
10	697459H1	219	1179-1387	SYNORAT03
11	3321983H1	279	1207-1485	PTHYNOT03
12	8576918T1	862	1176-1973	PENIFEC01

IN THE CLAIMS:

Claim 1 has been amended as follows:

1. (Once Amended) An isolated cDNA, or the complement thereof, comprising a nucleic acid sequence encoding a protein [having the] selected from :

a) amino acid sequence of SEQ ID NO:1;

b) an antigenic fragment of SEQ ID NO:1 from about amino acid residue P216 to about amino acid residue P235 of SEQ ID NO:1; and

c) a naturally occurring variant of the amino acid sequence of SEQ ID NO:1 having at least 95% identity to SEQ ID NO:1[, or the complement of the cDNA].